

SEQUENCE LISTING

<110> Jing, Shuqian

<120> IL-17 Receptor Like Molecules and Uses Thereof

<130> 01017/39525

<140> To be assigned
<141> Herewith

<150> 09/809,567

<151> 2001-03-15

<150> 09/724,460

<151> 2000-11-28

<150> 60/189,816

<151> 2000-03-16

<160> 19

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<221> CDS

<222> (22)..(2235)

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Phe Phe Thr Val Asn Ala Cys Léu Asn Gly Ser Gln Leu Ala Val Ala
15 20 25

gct ggc ggg tcc ggc cgc gcg tgg ggc gtc gac acc tgt ggc tgg agg
Ala Gly Gly Ser Gly Arg Ala Trp Gly Val Asp Thr Cys Gly Trp Arg
30 35 40

gga gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc
Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe
45 50 55

aaa tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg
Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val
60 65 70

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Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp
75 80 85 90

caa gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa
Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu
95 100 105

51

99

147

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243

291

339

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Arg	Gln	Cys	Gln	Gln	Leu	Ile	Leu	Lys	Asp	Pro	Lys	Gln	Leu	Asn	Ser	
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Ser	Phe	Lys	Arg	Thr	Gly	Met	Glu	Ser	Gln	Pro	Phe	Leu	Asn	Met	Lys	
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aac	gaa	agc	aat	tac	cac	cct	ttc	ttc	ttt	aga	acc	cga	gcc	tgt	gac	579
Asn	Glu	Ser	Asn	Tyr	His	Pro	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp		
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ctg	ttg	tta	cag	ccg	gac	aat	cta	gct	tgt	aaa	ccc	ttc	tgg	aag	cct	627
Leu	Leu	Leu	Gln	Pro	Asp	Asn	Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	
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Asp	His	Ala	Pro	His	Asn	Phe	Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	
						220			225			230				
aag	ctc	aag	cac	gaa	gga	cct	ttc	aag	cga	aag	acc	tgt	aag	cag	gag	771
Lys	Leu	Lys	His	Glu	Gly	Pro	Phe	Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	
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caa	act	aca	gag	acg	acc	agc	tgc	ctc	ctt	caa	aat	gtt	tct	cca	ggg	819
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Met	His	Tyr	Ala	Leu	Lys	Pro	Val	His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	
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Thr	Leu	Phe	Thr	Val	Met	Cys	Arg	Lys	Lys	Gln	Gln	Glu	Asn	Ile	Tyr	
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tca	cat	tta	gat	gaa	gag	agc	tct	gag	tct	tcc	aca	tac	act	gca	gca	1059
Ser	His	Leu	Asp	Glu	Glu	Ser	Ser	Glu	Ser	Ser	Thr	Thr	Tyr	Thr	Ala	
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ctc	cca	aga	gag	agg	ctc	cg	ccg	ccg	ccg	aag	gtc	ttt	ctc	tgc	tat	1107
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tac ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg	1203
Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp	
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Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln	
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Lys Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met	
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Lys Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Arg	
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Gly Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala	
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Ile Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln	
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Leu Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly	
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Gln His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser	
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Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp	
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Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro	
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575 580 585	
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Val Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys	
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Ser Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser
685 690 695

tct tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc 2163
Ser Ser Gly Leu Gly Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu
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ctc tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act 2211
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715 720 725 730

gat gaa ctc cac gcg gtc gcc cct ttgttaacaaa acgaaagagt ctaaggattg 2265
Asp Glu Leu His Ala Val Ala Pro
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Ala Trp Gly Val Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser
35 40 45

Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
50 55 60

Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
65 70 75 80

Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
85 90 95

Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
100 105 110

Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu
115 120 125

Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly
130 135 140

Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
145 150 155 160

Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His
165 170 175

Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp
180 185 190

Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser
195 200 205

Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn
210 215 220

Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly
225 230 235 240

Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr
245 250 255

Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu
260 265 270

Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys
275 280 285

Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Met Ala Ile Thr
290 295 300

Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
305 310 315 320

Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
325 330 335

Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu
340 345 350

Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
355 360 365

Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
370 375 380

Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
385 390 395 400

Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln
405 410 415

Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
420 425 430

Lys Asn Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu
435 440 445

Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
450 455 460

Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe
465 470 475 480

Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
485 490 495

Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
500 505 510

Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
515 520 525

Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val
530 535 540

Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe
545 550 555 560

Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu
565 570 575

Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met
580 585 590

Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Pro
595 600 605

Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
610 615 620

Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser
625 630 635 640

Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
645 650 655

Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
660 665 670

Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
675 680 685

Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu
690 695 700

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705 710 715 720

Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val
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Ala Pro

<210> 3

<211> 810

<212> PRT

<213> Homo sapiens

<400> 3

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20 25 30

Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln Pro Gly Leu
35 40 45

Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
50 55 60

Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu
65 70 75 80

His Phe Ala His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile
85 90 95

Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
100 105 110

Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg
115 120 125

Phe Glu Phe Leu Ser Lys Leu Arg His His Arg Arg Trp Arg Phe
130 135 140

Thr Phe Ser His Phe Val Val Asp Pro Asp Gln Glu Tyr Glu Val Thr
145 150 155 160

Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln
165 170 175

Ser Lys Asn Phe Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val
180 185 190

Thr Thr Pro Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr
195 200 205

Val Glu Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp
210 215 220

Asn Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met
225 230 235 240

Glu Asn His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro Arg
245 250 255

Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu Arg Asn
260 265 270

Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser
275 280 285

Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr Val Ser Cys Pro
290 295 300

Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp Tyr Met Pro Leu Trp
305 310 315 320

Val Tyr Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val
325 330 335

Ile Leu Leu Ile Val Cys Met Thr Trp Arg Leu Ala Gly Pro Gly Ser
340 345 350

Glu Lys Tyr Ser Asp Asp Thr Lys Tyr Thr Asp Gly Leu Pro Ala Ala
355 360 365

Asp Leu Ile Pro Pro Pro Leu Lys Pro Arg Lys Val Trp Ile Ile Tyr
370 375 380

Ser Ala Asp His Pro Leu Tyr Val Asp Val Val Leu Lys Phe Ala Gln
385 390 395 400

Phe Leu Leu Thr Ala Cys Gly Thr Glu Val Ala Leu Asp Leu Leu Glu
405 410 415

Glu Gln Ala Ile Ser Glu Ala Gly Val Met Thr Trp Val Gly Arg Gln
420 425 430

Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Val Leu Cys Ser
435 440 445

Arg Gly Thr Arg Ala Lys Trp Gln Ala Leu Leu Gly Arg Gly Ala Pro
450 455 460

Val Arg Leu Arg Cys Asp His Gly Lys Pro Val Gly Asp Leu Phe Thr
465 470 475 480

Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro Ala Cys Phe
485 490 495

Gly Thr Tyr Val Val Cys Tyr Phe Ser Glu Val Ser Cys Asp Gly Asp
500 505 510

Val Pro Asp Leu Phe Gly Ala Ala Pro Arg Tyr Pro Leu Met Asp Arg
515 520 525

Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met Phe Gln Pro
530 535 540

Gly Arg Met His Arg Val Gly Glu Leu Ser Gly Asp Asn Tyr Leu Arg
545 550 555 560

Ser Pro Gly Gly Arg Gln Leu Arg Ala Ala Leu Asp Arg Phe Arg Asp
565 570 575

Trp Gln Val Arg Cys Pro Asp Trp Phe Glu Cys Glu Asn Leu Tyr Ser
580 585 590

Ala Asp Asp Gln Asp Ala Pro Ser Leu Asp Glu Glu Val Phe Glu Glu
595 600 605

Pro Leu Leu Pro Pro Gly Thr Gly Ile Val Lys Arg Ala Pro Leu Val
610 615 620

Arg Glu Pro Gly Ser Gln Ala Cys Leu Ala Ile Asp Pro Leu Val Gly
625 630 635 640

Glu Glu Gly Ala Ala Val Ala Lys Leu Glu Pro His Leu Gln Pro
645 650 655

Arg Gly Gln Pro Ala Pro Gln Pro Leu His Thr Leu Val Leu Ala Ala
660 665 670

Glu Glu Gly Ala Leu Val Ala Ala Val Glu Pro Gly Pro Leu Ala Asp
675 680 685

Gly Ala Ala Val Arg Leu Ala Leu Ala Gly Glu Gly Glu Ala Cys Pro
690 695 700

Leu Leu Gly Ser Pro Gly Ala Gly Arg Asn Ser Val Leu Phe Leu Pro
705 710 715 720

Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Ser Thr Pro Met Ala Ser
725 730 735

Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met
740 745 750

Leu Ser Leu Phe Glu Gln Ser Leu Ser Cys Gln Ala Gln Gly Gly Cys
755 760 765

Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu
770 775 780

Glu Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser
785 790 795 800

Ser Pro Gln Pro Pro Glu Gly Leu Thr Glu
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<223> Description of Artificial Sequence: Primer 2417-51

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<210> 5
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<210> 6
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<223> Description of Artificial Sequence: Primer 2418-64

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cgtggtcgaa ggacacctgc atg 23

<210> 7
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<210> 8
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<210> 14
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<212> PRT
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<210> 18
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(959)

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Ser Gly Gln Lys Glu Arg Trp Met Met Ser Gly Asp
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Trp His Asp Pro Gly Ser Gln Gln Cys Cys Leu His Leu Asp Ser Met
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Gly Leu Cys Val Gly Arg Ala Asn Trp Leu His Ser Ala Ser Cys Ser
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Leu Val Phe Pro Gln Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu
45 50 55 60

tac aac atc acc ttc aaa tat gac aat tgt acc acc tac ttg aat cca 302
Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro
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Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln
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Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly
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Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu
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Iys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro
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Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro
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Thr Arg Ala Cys Asp Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys
190 195 200

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Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp
205 210 215 220

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Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe
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Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys
240 245 250

acc tgt aag cag gag caa act aca gag atg acc agc tgc ctc ctt caa 878
Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser Cys Leu Leu Gln
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Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn
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35 40 45

Gln Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr
50 55 60

Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His
65 70 75 80

Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His
85 90 95

Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile
100 105 110

Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu
115 120 125

Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn
130 135 140

Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met
145 150 155 160

Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile
165 170 175

Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys
180 185 190

Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys
195 200 205

Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser
210 215 220

Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His
225 230 235 240

Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln
245 250 255

Glu Gln Thr Thr Glu Met Thr Ser Cys Leu Leu Gln Asn Val Ser Pro
260 265 270

Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys
275 280 285

Val Met His Tyr Ala Leu Lys Pro
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